

### Amendments to the Specification

(1) Please replace the existing paper and electronic versions of Sequence Listing with the enclosed Replacement Sequence Listing (15 pages) and computer-readable Sequence Listing on diskette.

(2) Please amend the paragraph beginning at page 4, line 15, as follows:

FIG. 3 shows amino acid sequence similarities between the *Euglena*  $\Delta^8$ -desaturase protein (EFD1) (SEQ ID NO: 4) and the desaturase enzymes of *C. elegans*. The deduced amino acid sequence of the *EFD1* gene shows similarity with the *C. elegans*  $\Delta^6$  (FAT-3) (SEQ ID NO: 14) and  $\Delta^5$  (FAT-4) (SEQ ID NO: 2) desaturases (Napier et al., *Biochem. J.* **330**:611-614, 1998). The similarity is strongest in the regions of conserved function. In the N-terminal region amino acids forming a cytochrome  $b_5$  -like domain (Lederer, *Biochimie* **76**:674-692, 1994) are indicated. The His-box motifs indicated by underlined characters are present in other identified membrane desaturases (Napier et al., *Biochem. J.* **330**:611-614, 1998; Michaelson et al., *J. Biol. Chem.* **273**:19055-19059, 1998; and Shanklin and Cahoon, *Annu. Rev. Plant Physiol. Plant Mol. Biol.* **48**:611-641, 1998).

(3) Please amend the paragraph beginning at page 5, line 1, as follows:

FIG. 6A shows the primary amino acid sequence of the fatty acid  $\Delta^5$ -desaturase from *Caenorhabditis elegans* (SEQ ID NO: 2).

(4) Please amend the paragraph beginning at page 5, line 3, as follows:

FIG. 6B shows a nucleotide sequence including the ORF (open reading frame) that encodes the fatty acid  $\Delta^5$ -desaturase from *Caenorhabditis elegans* (SEQ ID NO: 1).

(5) Please amend the paragraph beginning at page 5, line 5, as follows:

FIG. 7A shows the primary amino acid sequence of the fatty acid  $\Delta^8$ -desaturase from the protist *Euglena gracilis* (SEQ ID NO: 4).

(6) Please amend the paragraph beginning at page 5, line 7, as follows:

FIG. 7B shows a nucleotide sequence including the ORF that encodes the  $\Delta^8$ -desaturase from the protist *Euglena gracilis* (SEQ ID NO: 3).

(7) Please amend the paragraph beginning at page 5, line 15, as follows:

FIG. 9 shows a comparison of the predicted amino acid sequences of the borage  $\Delta^6$ -desaturase (bord6) (SEQ ID NO: 15), *C. elegans* FAT-3 (fat3) (SEQ ID NO: 14), *C. elegans* FAT-4 (fat4) (SEQ ID NO: 2), and the *Mortierella alpina*  $\Delta^5$ -(mord5) desaturase (SEQ ID NO: 16). Identical or conserved residues are shaded, and the conserved HPGG heme-binding domain and the conserved histidine boxes are underlined. Abbreviations: bord6 = *Borago officinalis*  $\Delta^6$ -desaturase (GenBank accession number U79010); fat4 = *C. elegans* FAT-4 desaturase; fat3 = *C. elegans*  $\Delta^6$  desaturase sequence of W08D2.4 (GenBank accession number Z70271), edited to remove amino acids 38-67, on the basis of the cDNA sequence; mord5 = *Mortierella alpina*  $\Delta^5$  desaturase (GenBank accession number AF054824).

### **Amendments to the Drawings**

The attached Replacement Drawing Sheet includes changes to FIG. 3. This sheet replaces the original sheet containing FIG. 3. In FIG. 3, the name and the sequence of efd1 (*Euglena*  $\Delta^8$ -desaturase protein; as set forth in SEQ ID NO: 4) have been corrected.

Attachment: Replacement Sheet  
Annotated Sheet Showing Changes